

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

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<151> 2004-07-29

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<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:
pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

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<221> CDS

<222> (1)..(1785)

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<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

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Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	
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Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	
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gga	gag	gag	ctg	ggc	agt	ggc	cag	ttt	gcc	atc	gtg	aag	aag	tgc	cgg	192
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	
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Glu	Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	
	65				70					75					80	

cag	agc	cgg	gcc	agc	cgt	cgg	ggc	gtg	tgc	cgg	gag	gaa	atc	gag	cgg	288
Gln	Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg	
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gag	gtg	agc	atc	ctg	cgg	cag	gtg	ctg	cac	ccc	aac	atc	atc	acg	ctg	336
Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	
			100					105					110			

cac	gac	gtc	tat	gag	aac	cgc	acc	gac	gtg	gtg	ctc	atc	ctt	gag	cta	384
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Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu	
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aac	atc	atg	tgt	tta	gac	aag	aat	atc	cca	att	cca	cac	atc	aag	ctg	576
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Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	
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Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	
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Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	
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ggc Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 565	atc Ile	aaa Lys	cgg Arg	gcg Ala	gcc Ala 570	gca Ala	ggg Gly	ccc Pro	gaa Glu	caa Gln 575	aaa Lys	1728
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 pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

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Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln
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Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu
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Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	Glu	Leu
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Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	Trp	Tyr
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 <223> immunoglobulin kappa chain leader sequence

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Gly Ser Thr Gly 20 Asp Ala Ala Gln Pro 25 Ala Met Ala Gln Val 30 Lys Leu

cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg 144
Gln Glu Ser 35 Gly Thr Glu Leu Ala 40 Lys Pro Gly Ala Ala 45 Val Lys Met

tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg 192
Ser Cys Lys 50 Ala Ser Gly Tyr 55 Thr Phe Thr Asp Tyr 60 Trp Met His Trp

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Val Lys Gln Arg Pro Gly 70 Gln Gly Leu Glu Trp 75 Ile Gly Tyr Ile Asn 80

cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc 288
Pro Asn Thr Ala Tyr 85 Thr Asp Tyr Asn Gln 90 Lys Phe Lys Asp Lys 95 Ala

aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc 336
Thr Leu Thr 100 Ala Asp Lys Ser Ser 105 Thr Ala Tyr Met Gln 110 Leu Arg

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Ser Leu Thr 115 Ser Glu Asp Ser Ala Val Tyr Tyr Cys 125 Ala Lys Lys Thr

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Thr Gln Thr Thr Trp Gly 135 Phe Pro Phe Trp Gly Gln 140 Gly Thr Thr Val

acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt 480
Thr Val Ser Ser Gly 150 Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly 160

ggc gga tcg gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg 528
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser 170 Pro Lys Ser Met Ala Met 175

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ctg Leu 210	ctg Leu	ata Ile	tac Tyr	ggg Gly	gcc Ala	tcc Ser 215	aac Asn	cgg Arg	tac Tyr	act Thr	ggg Gly 220	gtc Val	ccc Pro	gat Asp	cgc Arg	672
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gac Asp	ttt Phe 450	ggc Gly	ctg Leu	gct Ala	cac His	gaa Glu 455	ata Ile	gaa Glu	gat Asp	gga Gly	gtt Val 460	gaa Glu	ttt Phe	aaa Lys	aac Asn	1392

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Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr	
485 490 495	
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Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu	
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acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa ttc	1584
Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe	
515 520 525	
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565 570 575	
gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat	1776
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His	
580 585 590	
cat cat cat cat cat tga	1794
His His His His His	
595	

<210> 4
 <211> 597
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:
 pMS-(Ki-4-DAPK2')-II/G ORF

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 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
 20 25 30
 Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
 35 40 45
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
 50 55 60
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 65 70 75 80
 Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
 85 90 95
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
 100 105 110
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
 115 120 125
 Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
 130 135 140
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 145 150 155 160
 Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
 165 170 175
 Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
 180 185 190

Asp	Ser	Phe	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys
Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg
Phe	Ala	Gly	Ser	Gly	Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser
Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg
Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala
Ala	Ala	Leu	Glu	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	Asn
Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	Gly
Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	Glu
Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	Gln
Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg	Glu
Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	His
Asp	Leu	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu	Val
Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu	Ser
Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val	Asn
Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	Asn
Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu	Ile
Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys	Asn
Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr	Glu
Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	Tyr
Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	Glu
Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	Phe
Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	Leu
Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	His
Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Phe	Arg	Gly	Gly	Pro
Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His
His	His	His	His												

<210> 5

<211> 3102

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PMT-Ki-4
(scFv)-eEF-2K ORF

<220>

<221> CDS

<222> (1)..(3102)

<220>

<221> N_region
 <222> (2)..(22)
 <223> pelB leader sequence

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 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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 gcc cag ccg gcg atg gcc atg ggc cat cat cat cat cat cat cat cat 96
 Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His
 20 25 30
 cat cac agc agc ggc cat atc gac gac gac gac aag cat atg aag ctt 144
 His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu
 35 40 45
 atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act 192
 Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
 50 55 60
 gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct 240
 Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
 65 70 75 80
 ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct 288
 Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
 85 90 95
 gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat 336
 Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
 100 105 110
 act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac 384
 Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
 115 120 125
 aaa tcc tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag 432
 Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu
 130 135 140
 gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg 480
 Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp
 145 150 155 160
 ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt 528
 Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 165 170 175
 gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att 576
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Asp Ile
 180 185 190
 gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg 624
 Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg
 195 200 205
 gtc acc ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc 672
 Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser
 210 215 220
 tgg tat caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg 720
 Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly
 225 230 235 240
 gcc tcc aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga 768
 Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly
 245 250 255

tct Ser	gga Gly	aga Arg	gat Asp 260	ttc Phe	act Thr	ctg Leu	acc Thr	atc Ile 265	agc Ser	agt Ser	gtg Val	cag Gln	gct Ala 270	gaa Glu	gac Asp	816
ctt Leu	gca Ala	gat Asp 275	tat Tyr	cac His	tgt Cys	gga Gly	cag Gln 280	aat Asn	tac Tyr	agg Arg	tat Tyr	ccg Pro 285	ctc Leu	acg Thr	ttc Phe	864
ggt Gly	gct Ala 290	ggc Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 295	atc Ile	aaa Lys	cgg Arg	gcg Ala	gcc Ala 300	gca Ala	gag Glu	ctc Leu	ggc Gly	912
gga Gly 305	ggt Gly	ggc Gly	tct Ser	atg Met	gca Ala 310	gac Asp	gaa Glu	gat Asp	ctc Leu	atc Ile 315	ttc Phe	cgc Arg	ctg Leu	gaa Glu	ggc Gly 320	960
gtt Val	gat Asp	ggc Gly	ggc Gly	cag Gln 325	tcc Ser	ccc Pro	cga Arg	gct Ala	ggc Gly 330	cat His	gat Asp	ggt Gly	gat Asp	tct Ser 335	gat Asp	1008
ggg Gly	gac Asp	agc Ser	gac Asp 340	gat Asp	gag Glu	gaa Glu	ggt Gly	tac Tyr 345	ttc Phe	atc Ile	tgc Cys	ccc Pro	atc Ile 350	acg Thr	gat Asp	1056
gac Asp	cca Pro	agc Ser 355	tcg Ser	aac Asn	cag Gln	aat Asn	gtc Val 360	aat Asn	tcc Ser	aag Lys	gtt Val	aat Asn 365	aag Lys	tac Tyr	tac Tyr	1104
agc Ser	aac Asn 370	cta Leu	aca Thr	aaa Lys	agt Ser	gag Glu 375	cgg Arg	tat Tyr	agc Ser	tcc Ser	agc Ser 380	ggg Gly	tcc Ser	ccg Pro	gca Ala	1152
aac Asn 385	tcc Ser	ttc Phe	cac His	ttc Phe	aag Lys 390	gaa Glu	gcc Ala	tgg Trp	aag Lys	cac His 395	gca Ala	atc Ile	cag Gln	aag Lys	gcc Ala 400	1200
aag Lys	cac His	atg Met	ccc Pro	gac Asp 405	ccc Pro	tgg Trp	gct Ala	gag Glu	ttc Phe 410	cac His	ctg Leu	gaa Glu	gat Asp	att Ile 415	gcc Ala	1248
acc Thr	gaa Glu	cgt Arg	gct Ala 420	act Thr	cga Arg	cac His	agg Arg	tac Tyr 425	aac Asn	gcc Ala	gtc Val	acc Thr	ggg Gly 430	gaa Glu	tgg Trp	1296
ctg Leu	gat Asp	gat Asp 435	gaa Glu	gtt Val	ctg Leu	atc Ile	aag Lys 440	atg Met	gca Ala	tct Ser	cag Gln	ccc Pro 445	ttc Phe	ggc Gly	cga Arg	1344
gga Gly 450	gca Ala	atg Met	agg Arg	gag Glu	tgc Cys	ttc Phe 455	cgg Arg	acg Thr	aag Lys	aag Lys	ctc Leu 460	tcc Ser	aac Asn	ttc Phe	ttg Leu	1392
cat His 465	gcc Ala	cag Gln	cag Gln	tgg Trp	aag Lys 470	ggc Gly	gcc Ala	tcc Ser	aac Asn	tac Tyr 475	gtg Val	gcg Ala	aag Lys	cgc Arg	tac Tyr 480	1440
atc Ile	gag Glu	ccc Pro	gta Val	gac Asp 485	cgg Arg	gat Asp	gtg Val	tac Tyr	ttt Phe 490	gag Glu	gac Asp	gtg Val	cgt Arg	cta Leu 495	cag Gln	1488
atg Met	gag Glu	gcc Ala	aag Lys 500	ctc Leu	tgg Trp	ggg Gly	gag Glu	gag Glu 505	tat Tyr	aat Asn	cgg Arg	cac His	aag Lys 510	ccc Pro	ccc Pro	1536
aag Lys	cag Gln	gtg Val 515	gac Asp	atc Ile	atg Met	cag Gln	atg Met 520	tgc Cys	atc Ile	atc Ile	gag Glu	ctg Leu 525	aag Lys	gac Asp	aga Arg	1584
ccg Gly	ggc Gly	aag Arg	ccc Pro	ctc Leu	ttc Phe	cac His	ctg Leu	gag Glu	cac His	tac Tyr	atc Ile	gag Glu	ggc Gly	aag Arg	tac Tyr	1632

Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr	
530						535					540					
atc	aag	tac	aac	tcc	aac	tct	ggc	ttt	gtc	cgc	gat	gac	aac	atc	cgc	1680
Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg	
545					550					555					560	
ctg	acg	ccg	cag	gcc	ttc	agc	cac	ttc	act	ttt	gag	cgt	tcc	ggc	cat	1728
Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	
				565					570					575		
cag	ctg	ata	gtg	gtg	gac	atc	cag	gga	gtt	ggg	gat	ctc	tac	act	gac	1776
Gln	Leu	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp	
			580					585					590			
cca	cag	atc	cac	acg	gag	acg	ggc	act	gac	ttt	gga	gac	ggc	aac	cta	1824
Pro	Gln	Ile	His	Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	Gly	Asn	Leu	
		595					600					605				
ggc	gtc	cgc	ggg	atg	gag	ctc	ttc	ttc	tac	tct	cat	gcc	tgc	aac	cgg	1872
Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	Cys	Asn	Arg	
	610					615					620					
att	tgc	gag	agc	atg	ggc	ctt	gct	ccc	ttt	gac	ctc	tcg	ccc	cgg	gag	1920
Ile	Cys	Glu	Ser	Met	Gly	Leu	Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu	
625					630					635					640	
agg	gat	gca	gtg	aat	cag	aac	acc	aag	ctg	ctg	caa	tca	gcc	aag	acc	1968
Arg	Asp	Ala	Val	Asn	Gln	Asn	Thr	Lys	Leu	Leu	Gln	Ser	Ala	Lys	Thr	
				645					650					655		
atc	ttg	aga	gga	aca	gag	gaa	aaa	tgt	ggg	agc	ccc	cga	gta	agg	acc	2016
Ile	Leu	Arg	Gly	Thr	Glu	Glu	Lys	Cys	Gly	Ser	Pro	Arg	Val	Arg	Thr	
			660					665					670			
ctc	tct	ggg	agc	cgg	cca	ccc	ctg	ctc	cgt	ccc	ctt	tca	gag	aac	tct	2064
Leu	Ser	Gly	Ser	Arg	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Ser	Glu	Asn	Ser	
		675					680					685				
gga	gac	gag	aac	atg	agc	gac	gtg	acc	ttc	gac	tct	ctc	cct	tct	tcc	2112
Gly	Asp	Glu	Asn	Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser	
	690					695					700					
cca	tct	tcg	gcc	aca	cca	cac	agc	cag	aag	cta	gac	cac	ctc	cat	tgg	2160
Pro	Ser	Ser	Ala	Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp	
705					710					715					720	
cca	gtc	ttc	agt	gac	ctc	gat	aac	atg	gca	tcc	aga	gac	cat	gat	cat	2208
Pro	Val	Phe	Ser	Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His	
				725					730					735		
cta	gac	aac	cac	cgg	gag	tct	gag	aat	agt	ggg	gac	agc	gga	tac	ccc	2256
Leu	Asp	Asn	His	Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro	
			740					745					750			
agt	gag	aag	cgg	ggt	gag	ctg	gat	gac	cct	gag	ccc	cga	gaa	cat	ggc	2304
Ser	Glu	Lys	Arg	Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly	
		755					760					765				
cac	tca	tac	agt	aat	cgg	aag	tac	gag	tct	gac	gaa	gac	agc	ctg	ggc	2352
His	Ser	Tyr	Ser	Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly	
	770					775					780					
agc	tct	gga	cgg	gta	tgt	gta	gag	aag	tgg	aat	ctc	ctc	aac	tcc	tcc	2400
Ser	Ser	Gly	Arg	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser	
785					790					795					800	
cgc	ctc	cac	ctg	ccg	agg	gct	tcg	gcc	gtg	gcc	ctg	gaa	gtg	caa	agg	2448
Arg	Leu	His	Leu	Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg	

805										810					815					
ctt	aat	gct	ctg	gac	ctc	gaa	aag	aaa	atc	ggg	aag	tcc	att	ttg	ggg	2496				
Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly					
			820					825					830							
aag	gtc	cat	ctg	gcc	atg	gtg	cgc	tac	cac	gag	ggg	ggg	cgc	ttc	tgc	2544				
Lys	Val	His	Leu	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys					
		835					840					845								
gag	aag	ggc	gag	gag	tgg	gac	cag	gag	tcg	gct	gtc	ttc	cac	ctg	gag	2592				
Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu					
	850					855					860									
cac	gca	gcc	aac	ctg	ggc	gag	ctg	gag	gcc	atc	gtg	ggc	ctg	gga	ctc	2640				
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu					
					870					875					880					
atg	tac	tcg	cag	ttg	cct	cat	cac	atc	cta	gcc	gat	gtc	tct	ctg	aag	2688				
Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys					
				885					890					895						
gag	aca	gaa	gag	aac	aaa	acc	aaa	gga	ttt	gat	tac	tta	cta	aag	gcc	2736				
Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala					
			900					905					910							
gct	gaa	gct	ggc	gac	agg	cag	tcc	atg	atc	cta	gtg	gcg	cga	gct	ttt	2784				
Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe					
		915					920					925								
gac	tct	ggc	cag	aac	ctc	agc	ccg	gac	agg	tgc	caa	gac	tgg	cta	gag	2832				
Asp	Ser	Gly	Gln	Asn	Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Leu	Glu					
	930					935					940									
gcc	ctg	cac	tgg	tac	aac	act	gcc	ctg	gag	atg	acg	gac	tgt	gat	gag	2880				
Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu					
					950					955					960					
ggc	ggg	gag	tac	gac	gga	atg	cag	gac	gag	ccc	cgg	tac	atg	atg	ctg	2928				
Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu					
				965					970					975						
gcc	agg	gag	gcc	gag	atg	ctg	ttc	aca	gga	ggc	tac	ggg	ctg	gag	aag	2976				
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys					
			980					985					990							
gac	ccg	cag	aga	tca	ggg	gac	ttg	tat	acc	cag	gca	gca	gag	gca	gcg	3024				
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala					
		995					1000				1005									
atg	gaa	gcc	atg	aag	ggc	cga	ctg	gcc	aac	cag	tac	tac	caa	aag	gct	3072				
Met	Glu	Ala	Met	Lys	Gly	Arg	Leu	Ala	Asn	Gln	Tyr	Tyr	Gln	Lys	Ala					
	1010					1015					1020									
gaa	gag	gcc	tgg	gcc	cag	atg	gag	gag	taa							3102				
Glu	Glu	Ala	Trp	Ala	Gln	Met	Glu	Glu												
	1025				1030															

<210> 6

<211> 1033

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: PMT-Ki-4
(ScFv)-eEF-2K ORF

<400> 6

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Ala	Gln	Pro	Ala	Met	Ala	Met	Gly	His	His	His	His	His	His	His	His	His
His	His	Ser	Ser	Gly	His	Ile	Asp	Asp	Asp	Asp	Lys	His	Met	Lys	Leu	
Met	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	
Glu	Leu	Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	
Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	
Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	
Thr	Asp	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	
Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	
Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp	
Gly	Phe	Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	
Val	Leu	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg	
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	
Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly	
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	
Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe	
Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Glu	Leu	Gly	
Gly	Gly	Gly	Ser	Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly	
Val	Asp	Gly	Gly	Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp	
Gly	Asp	Ser	Asp	Asp	Glu	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp	
Asp	Pro	Ser	Ser	Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr	
Ser	Asn	Leu	Thr	Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala	
Asn	Ser	Phe	His	Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala	
Lys	His	Met	Pro	Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala	
Thr	Glu	Arg	Ala	Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp	
Leu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg	
Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu	
His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr	
Ile	Glu	Pro	Val	Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	Arg	Leu	Gln	
Met	Glu	Ala	Lys	Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	Lys	Pro	Pro	
Lys	Gln	Val	Asp	Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg	
Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr	
Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg	
Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	

Gln	Leu	Ile	Val	565 Val	Asp	Ile	Gln	Gly	570 Val	Gly	Asp	Leu	Tyr	575 Thr	Asp
Pro	Gln	Ile	580 His	Thr	Glu	Thr	Gly	585 Thr	Asp	Phe	Gly	Asp	590 Gly	Asn	Leu
Gly	Val	Arg	Gly	Met	Ala	Leu	600 Phe	Phe	Tyr	Ser	His	605 Ala	Cys	Asn	Arg
Ile	Cys	Glu	Ser	Met	Gly	Leu	615 Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu
625 Arg	Asp	Ala	Val	Asn	630 Gln	Asn	Thr	Lys	Leu	635 Leu	Gln	Ser	Ala	Lys	Thr
Ile	Leu	Arg	Gly	Thr	Glu	Glu	Lys	Cys	Gly	Ser	Pro	Arg	Val	Arg	Thr
Leu	Ser	Gly	Ser	Arg	Pro	Pro	Leu	650 Leu	Arg	Pro	Leu	Ser	655 Glu	Asn	Ser
Gly	Asp	Glu	Asn	Met	Ser	Asp	660 Val	Thr	Phe	Asp	Ser	Leu	665 Pro	Ser	Ser
Pro	Ser	Ser	Ala	Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp
705 Pro	Val	Phe	Ser	Asp	710 Leu	Asp	Asn	Met	Ala	715 Ser	Arg	Asp	His	Asp	His
Leu	Asp	Asn	His	Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro
Ser	Glu	Lys	Arg	Gly	Glu	Leu	Asp	745 Pro	Glu	Pro	Arg	Glu	His	Gly	
His	Ser	Tyr	Ser	Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly
Ser	Ser	Gly	Arg	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser
785 Arg	Leu	His	Leu	Pro	Arg	Ala	Ser	Ala	Val	795 Ala	Leu	Glu	Val	Gln	Arg
Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly
Lys	Val	His	Leu	Ala	Met	Val	Arg	825 Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys
Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu
865 Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys
Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala
Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	905 Met	Ile	Leu	Val	Ala	Arg	Ala	Phe
Asp	Ser	Gly	Gln	Asn	Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Leu	Glu
Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu
945 Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala
Met	Glu	Ala	Met	Lys	Gly	Arg	Leu	Ala	Asn	Gln	Tyr	Tyr	Gln	Lys	Ala
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1025					1030										

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<212> PRT

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linker

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domain IX of kinases

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1 5
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